

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Zabeau, Marc  
Vos, Pieter  
Simons, Guus

(ii) TITLE OF INVENTION: RESISTANCE AGAINST WILT INDUCING FUNGI

(iii) NUMBER OF SEQUENCES: 12

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SPENCER & FRANK  
(B) STREET: 1100 New York Avenue, N.W., Suite 300 East  
(C) CITY: Washington  
(D) STATE: DC  
(E) COUNTRY: USA  
(F) ZIP: 20005

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: PCT/EP96/03480  
(B) FILING DATE: 06-AUG-1996  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 95401849.5  
(B) FILING DATE: 07-AUG-1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Gollin, Michael A.  
(B) REGISTRATION NUMBER: 31,957  
(C) REFERENCE/DOCKET NUMBER: GUPLA 0008

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-414-4000  
(B) TELEFAX: 202-414-4040

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GACTGCGTAC CAATCNNN

19

## (2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GATGAGTCCT GAGTAANNN

19

## (2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTCGTAGACT GCGTACC

17

## (2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  
- (ii) MOLECULE TYPE: other nucleic acid
  - (A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AATTGGTACG CAGTCTAC

18

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs

- (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GACGATGAGT CCTGAG

16

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 14 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "oligonucleotide"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TACTCAGGAC TCAT

14

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 16 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GACTGCGTAC CAATTG

16

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 16 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid  
(A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GATGAGTCCT GAGTAA

16

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GACTGCGTAC CAATTCAAGA

19

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GATGAGTCCT GAGTAATCT

19

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6658 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1798..5595

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AAAAAAAGCAG CTTAAAAAAA AGTACTTKG AAAGGKGCTG AAACCTATT TTTGAAATAA	60
GCAGTTATGT GTTGGAAWA AAAGTGCTGA AGTTGCTATG TCAAACATGA AAAGGGRAAA	120
AATGGAAGAA AGAGWTGTTA GGGTTATGTC GTAATTGGA GATTGTATAA AAATATTAAG	180
GGCAAAAAAA ATAAAAATGT GTCAACTTAA AACAGCTTAT AAGCTAAAAG TTAAAAGCTG	240
GGGTAGAGGT GTTTTTTTT TTTTAGCTT ATAAGTTGTT TTAAGTTGAC CACATTTA	300
TTTTKTTGC CCTTAATATT TTTATACAAT CTCAAAATTA CGACATAACC CTAACATCTT	360
TTTCTCCCAT TTTTCCTTT TCACGTTGA CATAGCAACT TCAGCACTT TATCCAAACA	420
CATAACTGCT TATTTAAAAA ATAAGTTCA GCACTTCAA AAGTACTTT TTAAAGCTGC	480
TTTTATTAAG CCCATCCAAA CGGGCCCTAA AATTGCTAAT GTTGCTCTT TCTATTCTCA	540
AACTCCGTAA TATTTAAGAA AATTGCTAA TGATAGGTCA CTTTAACAC TAAATAATTA	600
TAAATTGGGT AGAAATTAT TTATCATTAA AAGCTTTTT AATTTGAGT CTTCTCCCTA	660
ATTAAGACCC TTCCCCTCTT GCTTCAATTAA TTTAACTGAA TAGTCTTGT CTTATTGTTG	720
GGTGAAAGTC TGTCTTCTTG TTAGGTACTA AGTCCTACAA TAATATCAAT AATTTGCTAT	780
GGAGAAAAAA ATATTATAGG AGAAAAATAA TTAATTTAA TTCATGAATA TGTCTTAATA	840
TGCAACTCAT TTTGCTTATA TATATCAAAT TAAACTCTGT TCCTTAACT TTTCCTATG	900
AAGATACATT TTAATTATT TGATGAGGTT AGTTTGAAA TTTATATTAT AATAATGAAA	960
TGATATAACT TAAAAGAAGT TGTTGATAT CTTATCAGAA TCATGCAGGT ACTCATAATA	1020
TAAGAAATAA TTATGATGAA ATTTATATAT GTTTATGCA GAGATTATT ACGCATTGTT	1080
TACTTGGGTT ATGTATTACT TATTCATCT TTTATCAGAA TGAAAATTA TCATTCAATA	1140
AGAAATCCAA TTCTGTTAAA TTCAAAATAC AAACAATAAC ATTTCAAGA CCGATTTTT	1200
GCCCAAGAAT ATACAGTAAA CATATTATG ATATGGTAGG TCTCTTAGT AATTGACCAA	1260
CAAGGATTGT GGTGGAGTGG GAAATACTCT TTAATACTTC ACCAAGAGGT CTCCAATTG	1320
AGCCCCGTGAA TACGAAATCG TCTTGTTAG TATATACCT AACCTAATAC AAAAATTAGT	1380
ATATTAGCCT TNACAGCTAA AATCTTGTG ACCTGTAAGT CACGCGAGGA CAAATTACC	1440
GTAACACCAA CTTATTCATG ATATAATTGT CCCTTTAGC ACGGTAATAA TGAGGTGGGT	1500
AGAAATTAT TACTTGAGGG CCCTTCTAC ACCCACCCCTT ATTCTCTTGC TTCAATTATT	1560
GAATTGAAGA AGTAATGAAA AACAGACTC CATTGGATAA AGGACAGTTT GCAAACACAG	1620
CTGTAACAAT TTAGAGCACT AGCAAAATAG AGAGAGTTT GAGAGAAATT TTTGTTGCA	1680
AATTACTCTT AACCTTCAGC AGGTAAAATA AAGTTCTTAA CTGAGACTAT TTGAAGATAT	1740
ATTTGTTAA AGAACATATT TGTGTGTTTC CTTGTTTGC TTTGCAGAT TTGAGAA	1797

ATG GAG ATT GGC TTA GCA GTT GGT GCA TTT CTC TCC TCA GCT TTG Met Glu Ile Gly Leu Ala Val Gly Gly Ala Phe Leu Ser Ser Ala Leu 1 5 10 15	1845
AAT GTT CTG TTT GAT AGG CTT GCT CCT AAC GGT GAT CTG CTC AAC ATG Asn Val Leu Phe Asp Arg Leu Ala Pro Asn Gly Asp Leu Leu Asn Met 20 25 30	1893
TTT CGG AAG CAT AAG GAT CAT GTT AAG CTC TTA AAG AAG CTG AAA ATG Phe Arg Lys His Lys Asp His Val Lys Leu Leu Lys Lys Leu Lys Met 35 40 45	1941
ACT TTG CGT GGT ATT CAG ATT GTG CTA AGT GAT GCA GAG AAT AAG CAA Thr Leu Arg Gly Ile Gln Ile Val Leu Ser Asp Ala Glu Asn Lys Gln 50 55 60	1989
GCA TCA AAT CCA TCT GTG AGA GAC TGG CTT AAT GAG CTT CGA GAT GCT Ala Ser Asn Pro Ser Val Arg Asp Trp Leu Asn Glu Leu Arg Asp Ala 65 70 75 80	2037
GTC GAC TCT GCT GAA AAT TTA ATA GAA GAA GTC AAT TAT GAA GCT TTG Val Asp Ser Ala Glu Asn Leu Ile Glu Glu Val Asn Tyr Glu Ala Leu 85 90 95	2085
AGG CTT AAG GTG GAA GGT CAG CAT CAG AAT TTT TCA GAA ACA AGC AAC Arg Leu Lys Val Glu Gly Gln His Gln Asn Phe Ser Glu Thr Ser Asn 100 105 110	2133
CAG CAA GTA AGT GAT GAT TTT TTC CTT AAC ATA AAG GAC AAG CTG GAA Gln Gln Val Ser Asp Asp Phe Phe Leu Asn Ile Lys Asp Lys Leu Glu 115 120 125	2181
GAC ACT ATT GAA ACA TTA AAG GAT TTG CAA GAG CAA ATT GGT CTC CTT Asp Thr Ile Glu Thr Leu Lys Asp Leu Gln Glu Gln Ile Gly Leu Leu 130 135 140	2229
GGC TTA AAG GAG TAT TTT GAT TCC ACG AAA CTA GAA ACT AGA AGA CCT Gly Leu Lys Glu Tyr Phe Asp Ser Thr Lys Leu Glu Thr Arg Arg Pro 145 150 155 160	2277
TCA ACT TCT GTG GAT GAT GAA TCT GAT ATC TTT GGT AGG CAG AGC GAA Ser Thr Ser Val Asp Asp Glu Ser Asp Ile Phe Gly Arg Gln Ser Glu 165 170 175	2325
ATA GAG GAT TTG ATT GAC CGT CTA TTG TCT GAA GGT GCA AGT GGG AAA Ile Glu Asp Leu Ile Asp Arg Leu Leu Ser Glu Gly Ala Ser Gly Lys 180 185 190	2373
AAG CTG ACA GTA GTT CCT ATC GTT GGA ATG GGC GGC CAG GGC AAG ACA Lys Leu Thr Val Val Pro Ile Val Gly Met Gly Gly Gln Gly Lys Thr 195 200 205	2421
ACA CTT GCT AAA GCC GTA TAC AAT GAT GAG AGG GTG AAG AAT CAT TTT Thr Leu Ala Lys Ala Val Tyr Asn Asp Glu Arg Val Lys Asn His Phe 210 215 220	2469
GAT TTG AAA GCG TGG TAT TGC GTT TCT GAA GGA TTT GAT GCT TTG AGA Asp Leu Lys Ala Trp Tyr Cys Val Ser Glu Gly Phe Asp Ala Leu Arg 225 230 235 240	2517

ATA ACA AAA GAA TTA CTC CAA GAA ATT GGC AAA TTT GAC TCG AAG GAT Ile Thr Lys Glu Leu Leu Gln Glu Ile Gly Lys Phe Asp Ser Lys Asp 245 250 255	2565
GTC CAC AAC AAT CTT AAC CAG CTT CAA GTC AAA TTG AAG GAA AGT TTG Val His Asn Asn Leu Asn Gln Leu Gln Val Lys Leu Lys Glu Ser Leu 260 265 270	2613
AAG GGA AAG AAG TTC CTT ATT GTT TTG GAT GAT GTG TGG AAT GAA AAT Lys Gly Lys Lys Phe Leu Ile Val Leu Asp Asp Val Trp Asn Glu Asn 275 280 285	2661
TAC AAC GAG TGG AAT GAC TTG AGA AAT ATT TTT GCA CAA GGA GAT ATA Tyr Asn Glu Trp Asn Asp Leu Arg Asn Ile Phe Ala Gln Gly Asp Ile 290 295 300	2709
GGA AGT AAG ATC ATT GTG ACG ACA CGC AAA GAC AGT GTT GCC TTG ATG Gly Ser Lys Ile Ile Val Thr Arg Lys Asp Ser Val Ala Leu Met 305 310 315 320	2757
ATG GGA AAT GAG CAA ATT CGC ATG GGC AAT TTG TCT ACC GAA GCC TCT Met Gly Asn Glu Gln Ile Arg Met Gly Asn Leu Ser Thr Glu Ala Ser 325 330 335	2805
TGG TCT TTA TTT CAA AGA CAT GCA TTT GAA AAC ATG GAT CCT ATG GGA Trp Ser Leu Phe Gln Arg His Ala Phe Glu Asn Met Asp Pro Met Gly 340 345 350	2853
CAT CCG GAA CTT GAA GAG GTC GGA AGA CAA ATT GCA GCC AAG TGC AAA His Pro Glu Leu Glu Val Gly Arg Gln Ile Ala Ala Lys Cys Lys 355 360 365	2901
GGA CTG CCC TTA GCT CTG AAG ACG CTC GCT GGC ATG TTA CGC TCC AAA Gly Leu Pro Leu Ala Leu Lys Thr Leu Ala Gly Met Leu Arg Ser Lys 370 375 380	2949
TCA GAG GTT GAA GAG TGG AAA CGT ATT TTG AGA AGT GAA ATA TGG GAG Ser Glu Val Glu Glu Trp Lys Arg Ile Leu Arg Ser Glu Ile Trp Glu 385 390 395 400	2997
CTG CCA CAC AAT GAC ATA TTA CCA GCG TTG ATG TTG AGC TAC AAT GAT Leu Pro His Asn Asp Ile Leu Pro Ala Leu Met Leu Ser Tyr Asn Asp 405 410 415	3045
CTT CCC GCA CAT TTA AAG CGA TGC TTT TCT TTT TGT GCA ATA TTT CCT Leu Pro Ala His Leu Lys Arg Cys Phe Ser Phe Cys Ala Ile Phe Pro 420 425 430	3093
AAA GAT TAT CCA TTT AGG AAA GAA CAA GTT ATT CAT CTA TGG ATT GCC Lys Asp Tyr Pro Phe Arg Lys Glu Gln Val Ile His Leu Trp Ile Ala 435 440 445	3141
AAT GGT CTC GTA CCA GTG AAA GAT GAA ATA AAT CAA GAT TTA GGC AAC Asn Gly Leu Val Pro Val Lys Asp Glu Ile Asn Gln Asp Leu Gly Asn 450 455 460	3189
CAA TAC TTT CTA GAG TTG AGA TCA AGA TCA TTA TTT GAA AAG GTC CCA Gln Tyr Phe Leu Glu Leu Arg Ser Arg Ser Leu Phe Glu Lys Val Pro 465 470 475 480	3237

AAT CCT TCT AAA AGG AAC ATA GAG GAA TTA TTC CTT ATG CAT GAC CTT Asn Pro Ser Lys Arg Asn Ile Glu Glu Leu Phe Leu Met His Asp Leu 485 490 495	3285
GTC AAT GAT TTA GCC CAA CTT GCA TCT TCA AAA CTT TGT ATC AGG TTA Val Asn Asp Leu Ala Gln Leu Ala Ser Ser Lys Leu Cys Ile Arg Leu 500 505 510	3333
GAA GAG AGC CAA GGA TCT CAT ATG TTG GAA CAA TGT CGG CAC TTA TCT Glu Glu Ser Gln Gly Ser His Met Leu Glu Gln Cys Arg His Leu Ser 515 520 525	3381
TAT TCA ATA GGA TTT AAT GGT GAG TTT AAG AAA TTG ACA CCC CTC TAC Tyr Ser Ile Gly Phe Asn Gly Glu Phe Lys Lys Leu Thr Pro Leu Tyr 530 535 540	3429
AAA TTG GAG CAG TTG AGG ACA TTG CTT CCG ATA CGT ATT GAA TTC AGA Lys Leu Glu Gln Leu Arg Thr Leu Leu Pro Ile Arg Ile Glu Phe Arg 545 550 555 560	3477
TTG CAC AAT CTA AGC AAG AGG GTG TTG CAT AAC ATA CTG CCT ACA CTA Leu His Asn Leu Ser Lys Arg Val Leu His Asn Ile Leu Pro Thr Leu 565 570 575	3525
AGA TCC TTG AGG GCC CTA TCA TTC TCT CAA TAC AAG ATT AAG GAG TTG Arg Ser Leu Arg Ala Leu Ser Phe Ser Gln Tyr Lys Ile Lys Glu Leu 580 585 590	3573
CCA AAT GAC TTG TTT ACC AAA TTA AAG CTC CTC AGA TTT TTG GAT ATT Pro Asn Asp Leu Phe Thr Lys Leu Lys Leu Arg Phe Leu Asp Ile 595 600 605	3621
TCT CGG ACA TGG ATT ACA AAG TTG CCG GAT TCC ATT TGT GGA TTA TAT Ser Arg Thr Trp Ile Thr Lys Leu Pro Asp Ser Ile Cys Gly Leu Tyr 610 615 620	3669
AAC TTG GAG ACA CTT CTC CTG TCA TCT TGT GCT GAT CTT GAG GAG CTA Asn Leu Glu Thr Leu Leu Ser Ser Cys Ala Asp Leu Glu Glu Leu 625 630 635 640	3717
CCG CTG CAG ATG GAG AAG TTG ATT AAC TTG CGT CAT CTT GAC GTA AGC Pro Leu Gln Met Glu Lys Leu Ile Asn Leu Arg His Leu Asp Val Ser 645 650 655	3765
AAC ACT CGG CGC TTG AAG ATG CCA CTA CAT CTG AGC AGG TTG AAA AGC Asn Thr Arg Arg Leu Lys Met Pro Leu His Leu Ser Arg Leu Lys Ser 660 665 670	3813
CTC CAA GTG TTG GTG GGA CCC AAG TTT TTT GTA GAT GGT TGG AGA ATG Leu Gln Val Leu Val Gly Pro Lys Phe Phe Val Asp Gly Trp Arg Met 675 680 685	3861
GAA GAT TTG GGT GAA GCA CAA AAC TTA CAT GGA TCT CTA TCA GTT GTG Glu Asp Leu Gly Glu Ala Gln Asn Leu His Gly Ser Leu Ser Val Val 690 695 700	3909
AAG TTG GAA AAT GTG GTT GAT AGA AGG GAA GCT GTG AAG GCA AAG ATG Lys Leu Glu Asn Val Val Asp Arg Arg Glu Ala Val Lys Ala Lys Met 705 710 715 720	3957

AGG GAG AAG AAT CAT GTT GAG CAA TTA TCA TTG GAG TGG AGT GAA AGT Arg Glu Lys Asn His Val Glu Gln Leu Ser Leu Glu Trp Ser Glu Ser 725 730 735	4005
AGT ATT GCC GAC AAT TCA CAA ACA GAA AGT GAC ATA CTT GAT GAG CTA Ser Ile Ala Asp Asn Ser Gln Thr Glu Ser Asp Ile Leu Asp Glu Leu 740 745 750	4053
TGC CCA CAT AAA AAC ATC AAA GTC GAA ATC AGT GGA TAT AGA GGG Cys Pro His Lys Asn Ile Lys Val Glu Ile Ser Gly Tyr Arg Gly 755 760 765	4101
ACA AAC TTT CCC AAT TGG GTA GCT GAT CCT TTG TTT CTT AAG CTG GTG Thr Asn Phe Pro Asn Trp Val Ala Asp Pro Leu Phe Leu Lys Leu Val 770 775 780	4149
AAT TTG TCT CTA AGA AAC TGC AAG GAC TGT TAC TCC TTG CCA GCA CTA Asn Leu Ser Leu Arg Asn Cys Lys Asp Cys Tyr Ser Leu Pro Ala Leu 785 790 795 800	4197
GGA CAA CTC CCT TGT TTG AAA TTC CTT TCC GTT AAA GGG ATG CAT GGA Gly Gln Leu Pro Cys Leu Lys Phe Leu Ser Val Lys Gly Met His Gly 805 810 815	4245
ATA AGA GTG GTG ACG GAA GAA TTC TAT GGC AGA TTG TCC TCC AAA AAG Ile Arg Val Val Thr Glu Glu Phe Tyr Gly Arg Leu Ser Ser Lys Lys 820 825 830	4293
CCT TTT AAC TCT CTA GAG AAG CTT GAA TTT GAA GAT ATG ACG GAG TGG Pro Phe Asn Ser Leu Glu Lys Leu Glu Phe Glu Asp Met Thr Glu Trp 835 840 845	4341
AAG CAA TGG CAC GCA CTA GGA ATT GGA GAG TTC CCT ACA CTT GAG AAC Lys Gln Trp His Ala Leu Gly Ile Gly Glu Phe Pro Thr Leu Glu Asn 850 855 860	4389
CTT TCA ATT AAA AAT TGC CCT GAG CTC AGT TTG GAG ATA CCC ATC CAA Leu Ser Ile Lys Asn Cys Pro Glu Leu Ser Leu Glu Ile Pro Ile Gln 865 870 875 880	4437
TTT TCA AGT TTA AAA AGG TTA GAA GTT AGT GAT TGT CCA GTT GTT TTT Phe Ser Ser Leu Lys Arg Leu Glu Val Ser Asp Cys Pro Val Val Phe 885 890 895	4485
GAT GAT GCC CAA CTG TTT AGA TCC CAA CTT GAG GCA ATG AAG CAG ATT Asp Asp Ala Gln Leu Phe Arg Ser Gln Leu Glu Ala Met Lys Gln Ile 900 905 910	4533
GAG GAA ATA GAT ATA TGT GAT TGT AAC TCT GTT ACC TCC TTT CCT TTT Glu Glu Ile Asp Ile Cys Asp Cys Asn Ser Val Thr Ser Phe Pro Phe 915 920 925	4581
AGC ATA CTG CCA ACT ACC TTG AAG AGA ATA CAG ATA TCT CGT TGC CCA Ser Ile Leu Pro Thr Thr Leu Lys Arg Ile Gln Ile Ser Arg Cys Pro 930 935 940	4629
AAA TTG AAA TTG GAG GCG CCA GTT GGT GAG ATG TTT GTG GAG TAT TTG Lys Leu Lys Leu Glu Ala Pro Val Gly Glu Met Phe Val Glu Tyr Leu 945 950 955 960	4677

AGA GTG AAT GAT TGT GGT TGT GTA GAT GAT ATA TCA CCT GAG TTT CTC Arg Val Asn Asp Cys Gly Cys Val Asp Asp Ile Ser Pro Glu Phe Leu 965 970 975	4725
CCA ACA GCA CGT CAA TTG AGT ATT GAA AAT TGC CAG AAC GTT ACT AGG Pro Thr Ala Arg Gln Leu Ser Ile Glu Asn Cys Gln Asn Val Thr Arg 980 985 990	4773
TTT TTG ATT CCT ACT GCC ACT GAA ACT CTC CGT ATT TCG AAT TGT GAG Phe Leu Ile Pro Thr Ala Thr Glu Thr Leu Arg Ile Ser Asn Cys Glu 995 1000 1005	4821
AAT GTT GAA AAA CTA TCG GTG GCA TGT GGA GGA GCG GCC CAG ATG ACG Asn Val Glu Lys Leu Ser Val Ala Cys Gly Ala Ala Gln Met Thr 1010 1015 1020	4869
TCA CTG AAT ATT TGG GGA TGT AAG AAG CTC AAG TGT CTT CCA GAA CTC Ser Leu Asn Ile Trp Gly Cys Lys Leu Lys Cys Leu Pro Glu Leu 1025 1030 1035 1040	4917
CTT CCA TCT CTC AAG GAA CTG CGT CTG TCT GAT TGT CCA GAA ATA GAA Leu Pro Ser Leu Lys Glu Leu Arg Leu Ser Asp Cys Pro Glu Ile Glu 1045 1050 1055	4965
GGA GAA TTG CCC TTC AAT TTA GAA ATA CTC CGT ATC ATA TAT TGC AAG Gly Glu Leu Pro Phe Asn Leu Glu Ile Leu Arg Ile Ile Tyr Cys Lys 1060 1065 1070	5013
AAA CTG GTG AAT GGC CGA AAG GAG TGG CAT TTA CAG AGA CTC ACA GAG Lys Leu Val Asn Gly Arg Lys Glu Trp His Leu Gln Arg Leu Thr Glu 1075 1080 1085	5061
TTA TGG ATC GAT CAT GAT GGG AGT GAC GAA GAT ATT GAA CAT TGG GAG Leu Trp Ile Asp His Asp Gly Ser Asp Glu Asp Ile Glu His Trp Glu 1090 1095 1100	5109
TTG CCT TGT TCT ATT CAG AGA CTT ACC ATA AAG AAT CTT AAA ACA TTA Leu Pro Cys Ser Ile Gln Arg Leu Thr Ile Lys Asn Leu Lys Thr Leu 1105 1110 1115 1120	5157
AGC AGC CAA CAT CTC AAA AGC CTC ACC TCT CTT CAA TAT CTA TGT ATT Ser Ser Gln His Leu Lys Ser Leu Thr Ser Leu Gln Tyr Leu Cys Ile 1125 1130 1135	5205
GAG GGT TAT TTA TCT CAG ATT CAG TCA CAA GGC CAG CTT TCC TCC TTT Glu Gly Tyr Leu Ser Gln Ile Gln Ser Gln Gly Gln Leu Ser Ser Phe 1140 1145 1150	5253
TCT CAC CTC ACT TCG CTT CAA ACT CTA CAA ATC TGG AAT TTC CTT AAT Ser His Leu Thr Ser Leu Gln Thr Leu Gln Ile Trp Asn Phe Leu Asn 1155 1160 1165	5301
CTC CAA TCA CTT GCT GAA TCA GCA CTG CCC TCC TCC CTC TCT CAC CTG Leu Gln Ser Leu Ala Glu Ser Ala Leu Pro Ser Ser Leu Ser His Leu 1170 1175 1180	5349
GAG ATA GAT GAT TGC CCT AAT CTC CAA TCA CTC TTC GAA TCA GCA CTG Glu Ile Asp Asp Cys Pro Asn Leu Gln Ser Leu Phe Glu Ser Ala Leu 1185 1190 1195 1200	5397

CCC TCC TCC CTC TCT CAG CTG TTC ATC CAG GAT TGC CCT AAT CTC CAA Pro Ser Ser Leu Ser Gln Leu Phe Ile Gln Asp Cys Pro Asn Leu Gln 1205 1210 1215	5445
TCC CTT CCA TTT AAA GGG ATG CCC TCT TCC CTC TCT AAA CTA TCT ATT Ser Leu Pro Phe Lys Gly Met Pro Ser Ser Leu Ser Lys Leu Ser Ile 1220 1225 1230	5493
TTC AAT TGC CCA TTG CTC ACA CCA CTA GAA TTT GAC AAG GGG GAA Phe Asn Cys Pro Leu Leu Thr Pro Leu Leu Glu Phe Asp Lys Gly Glu 1235 1240 1245	5541
TAC TGG CCA CAA ATT GCT CAT ATT CCC ATC ATA AAT ATC GAT TGG AAA Tyr Trp Pro Gln Ile Ala His Ile Pro Ile Ile Asn Ile Asp Trp Lys 1250 1255 1260	5589
TAT ATT TAACAATTAA AACAAATGGC TCTCCAATG ATGTAAGCTA TTCGTTACCC Tyr Ile 1265	5645
TTAGAAGCTT TTTATGATTC TATGTTCTC ATTGCTTATT GGTTTATGCT CTTACCGTGT	5705
TTTAATTCAC GTCTCAATTG CCACCATGTT TAATCGAAAG TTTTAGTTC TTGTAATCAT	5765
CAACCACCT ATGTCACTAG AAATTTGAT AGGTAAAAGA GGTAGACAAA AAAGCTAAC	5825
ATCTTTTTC TTTCGTATAG CGACCAAACA ACTACATTT GATAGGTAAG GGCTATAGAT	5885
ATACATTGC AGGGTGTAA ACCAAGGAGT AAGAAAATCA CTGTCTTCAG ATATCTTCTC	5945
TTGCATATAAC TTTGCAATT TTAAGCTACA TTTGAACTC ATGTGTTGTT GCTAACTTAA	6005
ACATGTTTG TGCTTAATCA GATGTGGATT TTGAAGAGCG AGTACGACAA GTCTGGTACA	6065
TTAATTGTCC GTAGAAGTGT TTCTAAGGTG CTGCTGCTAT TTTACATCT GTTCCCGAGT	6125
TTTGTTTTT TTTAAATCT TTCCACTAAA GCTATTATGT CGTCCACAGT GAATTTTCAG	6185
GTCTGTTGTT ATAGGCAAGT CTTGAGATG CGACTATCAA AGAAGGGCGA TTACAATCAG	6245
TGTACCGCTG AAACATTTC ATGTTCCAG TGCAAGCCTC TTTGTAAGT TGACAAACTC	6305
GATTAGTTAA TATGTTGGG ACTCAACTAG TGGTTAGAGT ACTCATTG TAAGACTTGT	6365
GTACAGAAAA TCAAATTAGA ATTATAACTC GTGATGGTTG AATAAACTCT AAGAAGTACT	6425
GATATATTTC TTAGTGGATA TGTTGTTGC TCATTCGGTG TTTGATATCC ACATTGGAGT	6485
CCAACAAAT TCGAATTGC ACAATCGAAG GAGCGGTGCT CCTGGCATGA TTTTTTCCC	6545
ATTCTACGAC TAGTGCTCCT AAATTCTAAT TAAGCATAGA AAAATCTCAA CTATCTCACC	6605
CAACTCATAT CAGGATAGAG TATTCCCTGA GGAGGATTCC TTCAGTTACA AAA	6658

## (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1266 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Glu	Ile	Gly	Leu	Ala	Val	Gly	Gly	Ala	Phe	Leu	Ser	Ser	Ala	Leu
1				5					10					15	
Asn	Val	Leu	Phe	Asp	Arg	Leu	Ala	Pro	Asn	Gly	Asp	Leu	Leu	Asn	Met
				20					25					30	
Phe	Arg	Lys	His	Lys	Asp	His	Val	Lys	Leu	Leu	Lys	Lys	Leu	Lys	Met
				35				40				45			
Thr	Leu	Arg	Gly	Ile	Gln	Ile	Val	Leu	Ser	Asp	Ala	Glu	Asn	Lys	Gln
					50		55				60				
Ala	Ser	Asn	Pro	Ser	Val	Arg	Asp	Trp	Leu	Asn	Glu	Leu	Arg	Asp	Ala
					65		70			75			80		
Val	Asp	Ser	Ala	Glu	Asn	Leu	Ile	Glu	Glu	Val	Asn	Tyr	Glu	Ala	Leu
					85				90				95		
Arg	Leu	Lys	Val	Glu	Gly	Gln	His	Gln	Asn	Phe	Ser	Glu	Thr	Ser	Asn
				100				105				110			
Gln	Gln	Val	Ser	Asp	Asp	Phe	Phe	Leu	Asn	Ile	Lys	Asp	Lys	Leu	Glu
				115				120				125			
Asp	Thr	Ile	Glu	Thr	Leu	Lys	Asp	Leu	Gln	Glu	Gln	Ile	Gly	Leu	Leu
				130				135				140			
Gly	Leu	Lys	Glu	Tyr	Phe	Asp	Ser	Thr	Lys	Leu	Glu	Thr	Arg	Arg	Pro
				145				150			155			160	
Ser	Thr	Ser	Val	Asp	Asp	Glu	Ser	Asp	Ile	Phe	Gly	Arg	Gln	Ser	Glu
					165				170				175		
Ile	Glu	Asp	Leu	Ile	Asp	Arg	Leu	Leu	Ser	Glu	Gly	Ala	Ser	Gly	Lys
				180				185				190			
Lys	Leu	Thr	Val	Val	Pro	Ile	Val	Gly	Met	Gly	Gly	Gln	Gly	Lys	Thr
				195				200				205			
Thr	Leu	Ala	Lys	Ala	Val	Tyr	Asn	Asp	Glu	Arg	Val	Lys	Asn	His	Phe
				210				215				220			
Asp	Leu	Lys	Ala	Trp	Tyr	Cys	Val	Ser	Glu	Gly	Phe	Asp	Ala	Leu	Arg
				225				230			235			240	
Ile	Thr	Lys	Glu	Leu	Leu	Gln	Glu	Ile	Gly	Lys	Phe	Asp	Ser	Lys	Asp
					245				250				255		
Val	His	Asn	Asn	Leu	Asn	Gln	Leu	Gln	Val	Lys	Leu	Lys	Glu	Ser	Leu
				260				265				270			
Lys	Gly	Lys	Lys	Phe	Leu	Ile	Val	Leu	Asp	Asp	Val	Trp	Asn	Glu	Asn
				275				280				285			
Tyr	Asn	Glu	Trp	Asn	Asp	Leu	Arg	Asn	Ile	Phe	Ala	Gln	Gly	Asp	Ile
				290				295				300			

Gly Ser Lys Ile Ile Val Thr Thr Arg Lys Asp Ser Val Ala Leu Met  
 305 310 315 320

Met Gly Asn Glu Gln Ile Arg Met Gly Asn Leu Ser Thr Glu Ala Ser  
 325 330 335

Trp Ser Leu Phe Gln Arg His Ala Phe Glu Asn Met Asp Pro Met Gly  
 340 345 350

His Pro Glu Leu Glu Glu Val Gly Arg Gln Ile Ala Ala Lys Cys Lys  
 355 360 365

Gly Leu Pro Leu Ala Leu Lys Thr Leu Ala Gly Met Leu Arg Ser Lys  
 370 375 380

Ser Glu Val Glu Glu Trp Lys Arg Ile Leu Arg Ser Glu Ile Trp Glu  
 385 390 395 400

Leu Pro His Asn Asp Ile Leu Pro Ala Leu Met Leu Ser Tyr Asn Asp  
 405 410 415

Leu Pro Ala His Leu Lys Arg Cys Phe Ser Phe Cys Ala Ile Phe Pro  
 420 425 430

Lys Asp Tyr Pro Phe Arg Lys Glu Gln Val Ile His Leu Trp Ile Ala  
 435 440 445

Asn Gly Leu Val Pro Val Lys Asp Glu Ile Asn Gln Asp Leu Gly Asn  
 450 455 460

Gln Tyr Phe Leu Glu Leu Arg Ser Arg Ser Leu Phe Glu Lys Val Pro  
 465 470 475 480

Asn Pro Ser Lys Arg Asn Ile Glu Glu Leu Phe Leu Met His Asp Leu  
 485 490 495

Val Asn Asp Leu Ala Gln Leu Ala Ser Ser Lys Leu Cys Ile Arg Leu  
 500 505 510

Glu Glu Ser Gln Gly Ser His Met Leu Glu Gln Cys Arg His Leu Ser  
 515 520 525

Tyr Ser Ile Gly Phe Asn Gly Glu Phe Lys Lys Leu Thr Pro Leu Tyr  
 530 535 540

Lys Leu Glu Gln Leu Arg Thr Leu Leu Pro Ile Arg Ile Glu Phe Arg  
 545 550 555 560

Leu His Asn Leu Ser Lys Arg Val Leu His Asn Ile Leu Pro Thr Leu  
 565 570 575

Arg Ser Leu Arg Ala Leu Ser Phe Ser Gln Tyr Lys Ile Lys Glu Leu  
 580 585 590

Pro Asn Asp Leu Phe Thr Lys Leu Lys Leu Leu Arg Phe Leu Asp Ile  
 595 600 605

Ser Arg Thr Trp Ile Thr Lys Leu Pro Asp Ser Ile Cys Gly Leu Tyr  
 610 615 620

Asn Leu Glu Thr Leu Leu Ser Ser Cys Ala Asp Leu Glu Glu Leu  
 625 630 635 640

Pro Leu Gln Met Glu Lys Leu Ile Asn Leu Arg His Leu Asp Val Ser  
 645 650 655

Asn Thr Arg Arg Leu Lys Met Pro Leu His Leu Ser Arg Leu Lys Ser  
 660 665 670

Leu Gln Val Leu Val Gly Pro Lys Phe Phe Val Asp Gly Trp Arg Met  
 675 680 685

Glu Asp Leu Gly Glu Ala Gln Asn Leu His Gly Ser Leu Ser Val Val  
 690 695 700

Lys Leu Glu Asn Val Val Asp Arg Arg Glu Ala Val Lys Ala Lys Met  
 705 710 715 720

Arg Glu Lys Asn His Val Glu Gln Leu Ser Leu Glu Trp Ser Glu Ser  
 725 730 735

Ser Ile Ala Asp Asn Ser Gln Thr Glu Ser Asp Ile Leu Asp Glu Leu  
 740 745 750

Cys Pro His Lys Asn Ile Lys Lys Val Glu Ile Ser Gly Tyr Arg Gly  
 755 760 765

Thr Asn Phe Pro Asn Trp Val Ala Asp Pro Leu Phe Leu Lys Leu Val  
 770 775 780

Asn Leu Ser Leu Arg Asn Cys Lys Asp Cys Tyr Ser Leu Pro Ala Leu  
 785 790 795 800

Gly Gln Leu Pro Cys Leu Lys Phe Leu Ser Val Lys Gly Met His Gly  
 805 810 815

Ile Arg Val Val Thr Glu Glu Phe Tyr Gly Arg Leu Ser Ser Lys Lys  
 820 825 830

Pro Phe Asn Ser Leu Glu Lys Leu Glu Phe Glu Asp Met Thr Glu Trp  
 835 840 845

Lys Gln Trp His Ala Leu Gly Ile Gly Glu Phe Pro Thr Leu Glu Asn  
 850 855 860

Leu Ser Ile Lys Asn Cys Pro Glu Leu Ser Leu Glu Ile Pro Ile Gln  
 865 870 875 880

Phe Ser Ser Leu Lys Arg Leu Glu Val Ser Asp Cys Pro Val Val Phe  
 885 890 895

Asp Asp Ala Gln Leu Phe Arg Ser Gln Leu Glu Ala Met Lys Gln Ile  
 900 905 910

Glu Glu Ile Asp Ile Cys Asp Cys Asn Ser Val Thr Ser Phe Pro Phe  
 915 920 925

Ser Ile Leu Pro Thr Thr Leu Lys Arg Ile Gln Ile Ser Arg Cys Pro  
 930 935 940

Lys Leu Lys Leu Glu Ala Pro Val Gly Glu Met Phe Val Glu Tyr Leu  
 945 950 955 960  
 Arg Val Asn Asp Cys Gly Cys Val Asp Asp Ile Ser Pro Glu Phe Leu  
 965 970 975  
 Pro Thr Ala Arg Gln Leu Ser Ile Glu Asn Cys Gln Asn Val Thr Arg  
 980 985 990  
 Phe Leu Ile Pro Thr Ala Thr Glu Thr Leu Arg Ile Ser Asn Cys Glu  
 995 1000 1005  
 Asn Val Glu Lys Leu Ser Val Ala Cys Gly Gly Ala Ala Gln Met Thr  
 1010 1015 1020  
 Ser Leu Asn Ile Trp Gly Cys Lys Lys Leu Lys Cys Leu Pro Glu Leu  
 1025 1030 1035 1040  
 Leu Pro Ser Leu Lys Glu Leu Arg Leu Ser Asp Cys Pro Glu Ile Glu  
 1045 1050 1055  
 Gly Glu Leu Pro Phe Asn Leu Glu Ile Leu Arg Ile Ile Tyr Cys Lys  
 1060 1065 1070  
 Lys Leu Val Asn Gly Arg Lys Glu Trp His Leu Gln Arg Leu Thr Glu  
 1075 1080 1085  
 Leu Trp Ile Asp His Asp Gly Ser Asp Glu Asp Ile Glu His Trp Glu  
 1090 1095 1100  
 Leu Pro Cys Ser Ile Gln Arg Leu Thr Ile Lys Asn Leu Lys Thr Leu  
 1105 1110 1115 1120  
 Ser Ser Gln His Leu Lys Ser Leu Thr Ser Leu Gln Tyr Leu Cys Ile  
 1125 1130 1135  
 Glu Gly Tyr Leu Ser Gln Ile Gln Ser Gln Gly Gln Leu Ser Ser Phe  
 1140 1145 1150  
 Ser His Leu Thr Ser Leu Gln Thr Leu Gln Ile Trp Asn Phe Leu Asn  
 1155 1160 1165  
 Leu Gln Ser Leu Ala Glu Ser Ala Leu Pro Ser Ser Leu Ser His Leu  
 1170 1175 1180  
 Glu Ile Asp Asp Cys Pro Asn Leu Gln Ser Leu Phe Glu Ser Ala Leu  
 1185 1190 1195 1200  
 Pro Ser Ser Leu Ser Gln Leu Phe Ile Gln Asp Cys Pro Asn Leu Gln  
 1205 1210 1215  
 Ser Leu Pro Phe Lys Gly Met Pro Ser Ser Leu Ser Lys Leu Ser Ile  
 1220 1225 1230  
 Phe Asn Cys Pro Leu Leu Thr Pro Leu Leu Glu Phe Asp Lys Gly Glu  
 1235 1240 1245

Tyr Trp Pro Gln Ile Ala His Ile Pro Ile Ile Asn Ile Asp Trp Lys  
1250 1255 1260

Tyr Ile  
1265